```
   1  ATGATGAGCT CCATGGTGAG GTTTAGCTCG AGCCCGTGCT CTTTCACCGG
  51  GTCGTTGTGC TCAACATCGC CGCAGTCGAT GCACCCCATG AGCTCTGTCG
 101  CGGCAAAGGT GACGAGGCAA TGTGGGTGCT TGAGAGCGGG GAATAAGCTG
 151  GATAAGGACC AATTTGTGGG TGATGGGAAA CCACTTATGC ATCAACAGAC
 201  GCGGGGATGG AGTCAGGGGC GGGAGAGGTG TCACGCAGGG AGGTCTGTGG
 251  TGATGGCCAG TATGAGTGGC GCCAAGATCA AGGTCATTGG TGTAGGCGGC
 301  GGGGGCAACA ATGCTGTGAA CCGCATGATT GGGAGCGGCA TTCAGGGTGT
 351  TGATTTTTGG GCCATCAACA CAGATGTTCA AGCTTTGCAG AAATCACAAG
 401  CCGAACATCG CGTTCAAATC GGCGAAGCTT TGACCCGAGG ACTTGGTACT
 451  GGTGGAAAGC CATTCCTTGG AGAACAAGCA GCAGAGGAAT CGATAGAAAT
 501  CATTGCACAG GCAGTGGTAG ATGCTGATCT TGTCTTCATT ACTGCGGGCA
 551  TGGGTGGTGG AACGGGGTCT GGGGCTGCCC CGGTCGTTGC CCGTGTGGCC
 601  AAAGAGGCAG GGCAACTCAC TGTTGGTGTT GTCACTTATC CGTTTACGTT
 651  TGAGGGCCGT CGGAGAAGCC AGCAGGCAGT GGAGGCAATA GAGAATCTGC
 701  GGAAGTCTGT CGACAGTCTT ATTGTCATTC CTAATGACCG TCTACTCGAT
 751  GTCTCCGGAG ATAAAACTCC TCTTCAGGAA GCATTTTCTC TAGCCGACGA
 801  TGTTCTTAGG CAGGGAGTTC AAGGCATTTC AGACATCATC ACAACGCCAG
 851  GTCTTGTGAA TGTTGATTTT GCAGATGTTA GAGCTGTAAT GAGTAACTCA
 901  GGTACAGCCA TGCTTGGCGT TGGCTCCTCT AGTGGCAAGA ATCGTGCTGA
 951  GGAGGCCGCT GTTCAAGCTG CTTCAGCCCC TCTTATTGAA CGCTCTATTG
1001  AACAAGCAAC TGGCATTGTA TACAACATCA CTGGTGGACC GGACCTCACA
1051  TTGCAGGAAG TCAACACCGT GTCTGAGATT GTAACAGGTT TAGCTGACCC
1101  CTCAGCTAAT ATCATTTTTG GAGCGGTAGT GGATGACAAA TATACAGGTG
1151  AAATCCATGT AACGATTATT GCCACGGGGT TCTCTCACAG TTTTCAGAAA
1201  TCACTAGTGG ACCCAAACGT TTCTAGGTCG GAGAGGCAGG ACGCCCCGAG
1251  TAATGCACTC GAGAAACCTT GGAAGCAACC AACTCCCACC TCATCAAGAT
1301  TTCGTCAAGG CCTTAATAGC AAGGGGTTTT TGTAG
```

Fig. 1

```
   1  ATGATCACGT GTAGGGTTTG GGTTGGTTTG GGGCCGGTGA GCCCTTCTTT
  51  GATTCTTCTG CCCTCGAAGA GTAACGGAGA ATGCGTCCTA AGTGCAAGAA
 101  AAGCTGATTG GGGATTACTG AGCCAAGTGC AATGCCAACG CTTTCGATGT
 151  CTATCTTCAG AATATAAGGG TCATAATCTT AAACTTAGAA GACGTAGCCG
 201  TGTCTCAGCT TCCAACAGAG AAAACGGTAG TTTAAATGGG CGTTTCCAGG
 251  AATCACTGAG TCAAGAGAAT GGGTATCCGG CACCAACTGA AGGGACTGAT
 301  CCTCACACTT TCTCCACGGC GATGGACTCC TTAGCTATTA AAGCAGAGGA
 351  AGCTTACAAT GACGTACAGG ATTCTTTTGC CAAGAGTAGT AAACAACGGA
 401  GCTTATCTGG CTGCGCTTCT ATCAAAGTGT TCGGTGTCGG GGGTGGTGGA
 451  TGCAATGCGG TAGACGAAAT GGTGAGGTCA GAACTATTGA ATGTTGAGTT
 501  CTGGGCCGTC AATACTGACA AACAAGCATT GAACAAGTCG CTGGCTCCCA
 551  ATAAAATTCA AATTGGACAG GACACGACAG CCGGCCGCGG TGCAGGTGGA
 601  AGAAGTGCAA CCGGTGAGGA AGCAGCTACA GAGTCATTGG CGGAGCTTTC
 651  GATGGCACTT GAAGGTGCCG ATTTAGTCTT CATCGCCTCC GGTATGGGTG
 701  GCGGTACTGG TTCAGGAGCA GCTCCTGTGG TGGCTCGGTT GGCGAAGGCT
 751  ATGGGAGCGT TAACGATTGG CATAGTAACT GAACCTTTCA CATTTGAAGG
 801  GTTCACCCGA GCTCGACAAG CTAGGAAAGC CATTGAGGAC ATGCGCCATG
 851  CGGCTGACAC TGTGGTTGTA GTTCCAAATG ATCGGTTGCT CCAGACTGTA
 901  GCACCTGACA CATCTATGCT GGAGGCTTTC CATCTTGCAG ATGACGTCTT
 951  GCGGCAGGGA GTGCAAGGAA TTTCAGACAT CATCACGATA CCCGGGCTAG
1001  TCAACGTCGA CTTTGCGGAT GTGAAAGCTA TCATGTCAAA TGCAGGGAGT
1051  GCAATGTTGG GAATCGGCGC TGGTTTTGGG AAGAAccgtg ctgagGAGGT
1101  GGCACGGTCA GCCATCATGT CTCCTCTACT CCGCTCCGTC TCGAGAcCCA
1151  TGGGTATTGT GTACAATGTG ACAGGTGGGA GCGACCTAAC TCTtcacgag
1201  gtcaACATCG CTGCCGAAAT TGTtCATGAC ATGGCTGATC CAAACGCAAA
1251  TGTTATCTTT GGGGCGGTCA TTGATGAGAG CTTTAAGGGG ATGATACGTA
1301  TGACTGTCAT TGCAACTGGA TTtAGAGAGC CTGGAGAGGA GAAGgTCGTT
1351  GgTAGTGTTC GAACTGTAGA CGATGATATA TTCTACTGGG AACAGAATAA
1401  GAATAGGTCC GACCTTGGCA AAGTGCCGGA CGTTTTGCGA AGAAAAGATC
1451  GAAGGCGTGG CAGTGGCAGG TAA
```

Fig. 2

```
  1  MMSSMVRFSS SPCSFTGSLC STSPQSMHPM SSVAAKVTRQ CGCLRAGNKL
 51  DKDQFVGDGK PLMHQQTRGW SQGRERCHAG RSVVMASMSG AKIKVIGVGG
101  GGNNAVNRMI GSGIQGVDFW AINTDVQALQ KSQAEHRVQI GEALTRGLGT
151  GGKPFLGEQA AEESIEIIAQ AVVDADLVFI TAGMGGGTGS GAAPVVARVA
201  KEAGQLTVGV VTYPFTFEGR RRSQQAVEAI ENLRKSVDSL IVIPNDRLLD
251  VSGDKTPLQE AFSLADDVLR QGVQGISDII TTPGLVNVDF ADVRAVMSNS
301  GTAMLGVGSS SGKNRAEEAA VQAASAPLIE RSIEQATGIV YNITGGPDLT
351  LQEVNTVSEI VTGLADPSAN IIFGAVVDDK YTGEIHVTII ATGFSHSFQK
401  SLVDPNVSRS ERQDAPSNAL EKPWKQPTPT SSRFRQGLNS KGFL
```

Fig. 3

```
  1  MITCRVWVGL GPVSPSLILL PSKSNGECVL SARKADWGLL SQVQCQRFRC
 51  LSSEYKGHNL KLRRRSRVSA SNRENGSLNG RFQESLSQEN GYPAPTEGTD
101  PHTFSTAMDS LAIKAEEAYN DVQDSFAKSS KQRSLSGCAS IKVFGVGGGG
151  CNAVDEMVRS ELLNVEFWAV NTDKQALNKS LAPNKIQIGQ DTTAGRGAGG
201  RSATGEEAAT ESLAELSMAL EGADLVFIAS GMGGGTGSGA APVVARLAKA
251  MGALTIGIVT EPFTFEGFTR ARQARKAIED MRHAADTVVV VPNDRLLQTV
301  APDTSMLEAF HLADDVLRQG VQGISDIITI PGLVNVDFAD VKAIMSNAGS
351  AMLGIALVLG KNRAEEVARS AIMSPLLRSV SRPMGIVYNV TGGSDLTLHE
401  VNIAAEIVHD MADPNANVIF GAVIDESFKG MIRMTVIATG FREPGEEKVV
451  GSVRTVDDDI FYWEQNKNRS DLGKVPDVLR RKDRRRGSGR
```

Fig. 4

```
108          MDS LAIKAEEAYN DVQDSFAKSS KQRSLSGCAS IKVFGVGGGG
151  CNAVDEMVRS ELLNVEFWAV NTDKQALNKS LAPNKIQIGQ DTTAGRGAGG
201  RSATGEEAAT ESLAELSMAL EGADLVFIAS GMGGGTGSGA APVVARLAKA
251  MGALTIGIVT EPFTFEGFTR ARQARKAIED MRHAADTVVV VPNDRLLQTV
301  APDTSMLEAF HLADDVLRQG VQGISDIITI PGLVNVDFAD VKAIMSNAGS
351  AMLGIALVLG KNRAEEVARS AIMSPLLRSV SRPMGIVYNV TGGSDLTLHE
401  VNIAAEIVHD MADPNANVIF GAVIDESFKG MIRMTVIATG FREPGEEKVV
451  GSVRTVDDDI FYWEQNKNRS DLGKVPDVLR RKDRRRGSGR
```

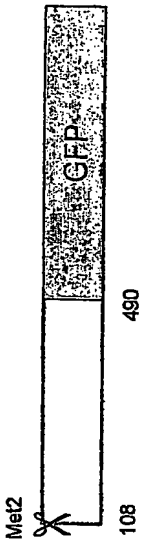
Fig. 5

Fig. 6a

FtsZ1-2

Fig. 6b

oder



FtsZ1-2/Met2

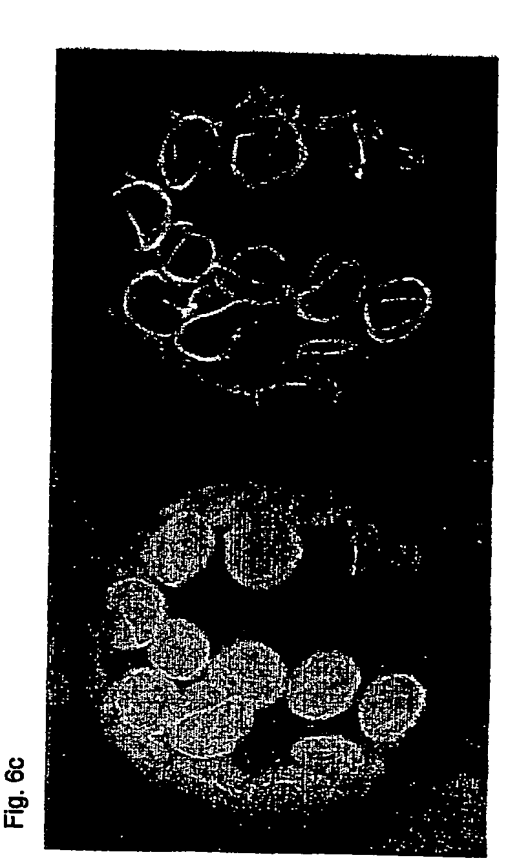
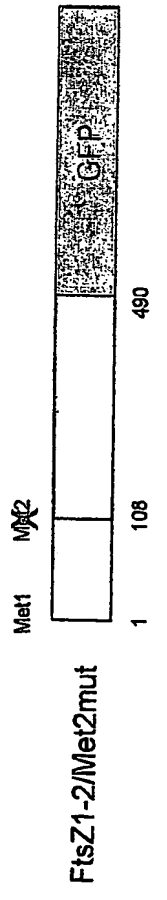


Fig. 6c



FtsZ1-2/Met2mut

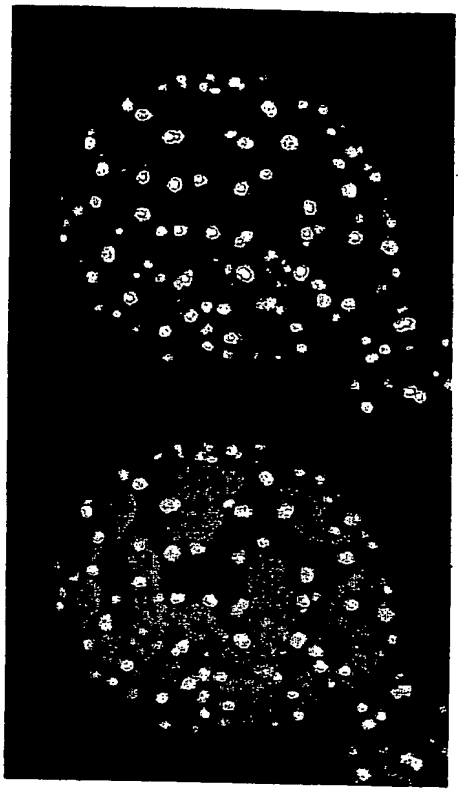
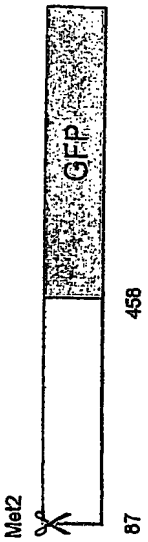


Fig. 6d



FtsZ2-1/Met2

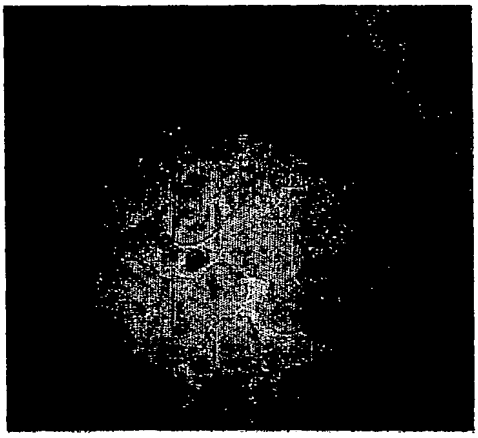


Fig. 7b

Fig. 7a

Fig.8 exon-intron structure

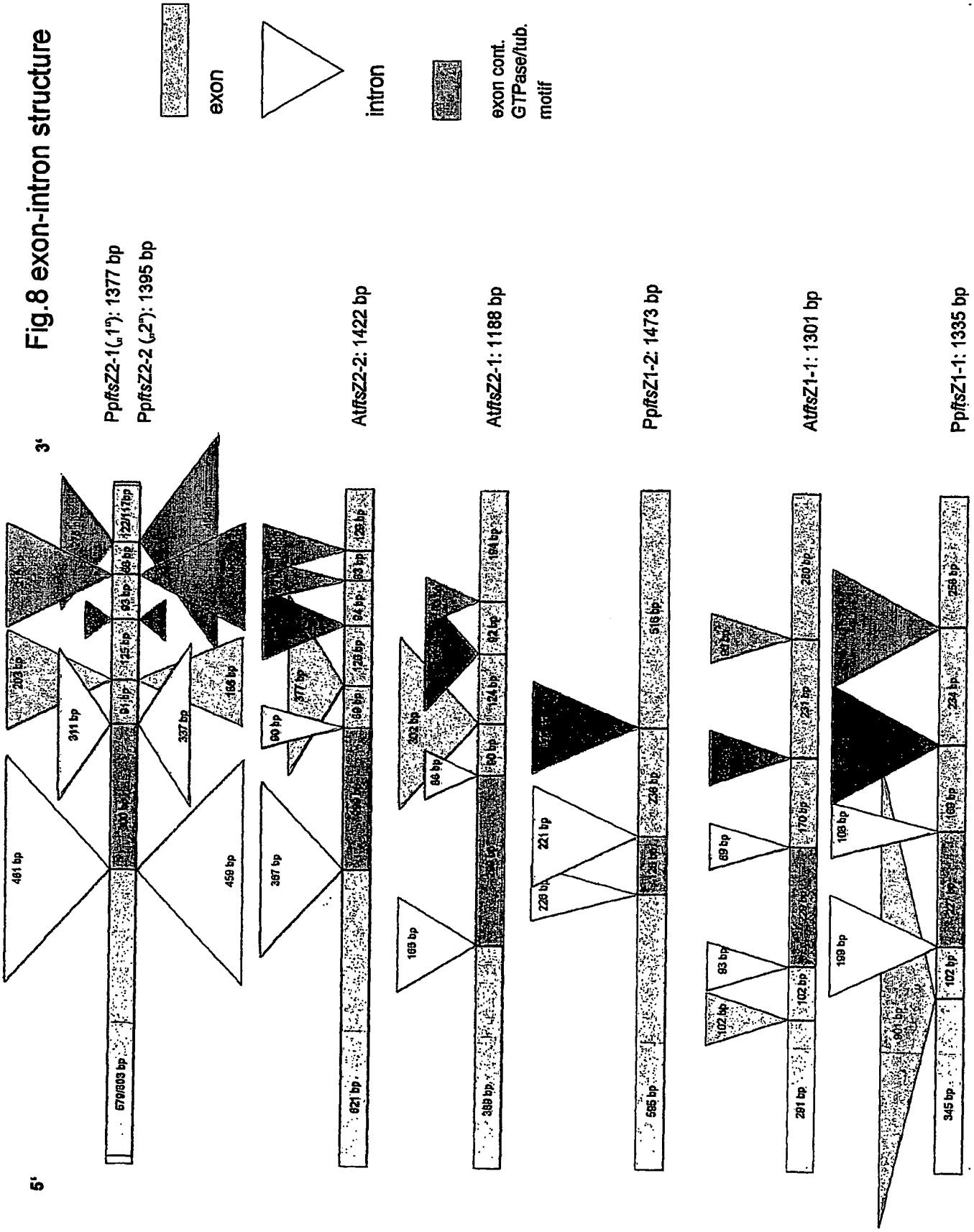
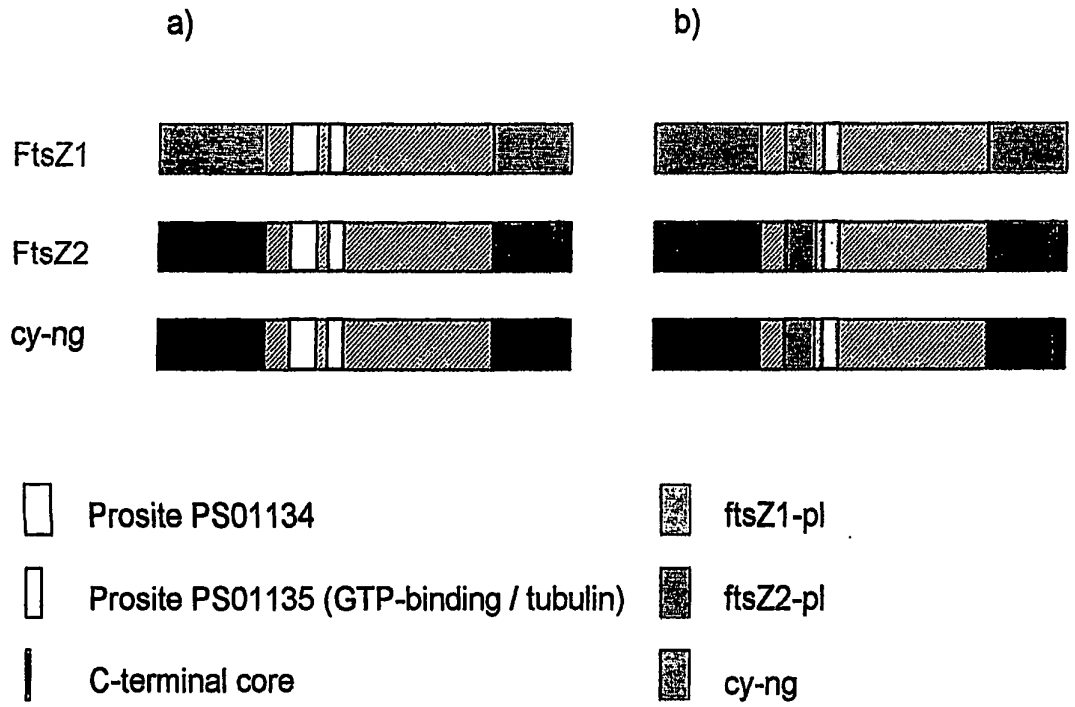


Fig.9

Schematic representation of FtsZ subfamilies and patterns, based on an alignment (580aa) of chlorobiont FtsZ proteins



d)

C-terminal core domain : (D,E)(I,V)Px(F,Y)L

```
FtsZ1
ARATH1-1        ----------STISTKSSSPRRLFF----------
PISSA           ----------SKVESRPPPPRKLFF----------
NICTA1-2        ----------STKPR--PATRRLFF----------
NICTA1-1        ----------STKPR--PAARRLFF----------
NICTA1-4        ----------STTSR--TPTRRLFF----------
NICTA1-3        ----------STTSR--TPTRRLFF----------
TAGER           ----------PAPSR----SRKLFF----------
ORYSA           ----------AATWS-----RRLFS----------
PHYPA3          ----------SSRFR-QGLNSKGFL----------
PHYPA4          ----------SDLGKVPDVLRRKDRRRGSGR----

FtsZ2
ARATH2-1        ----------SGSVEIPEFLKKKGSSRYPRV----
ARATH2-2        ----------GSSIEIPEFLKKKGRSRYPRL----
NICTA2-1        ----------GGSVEIPEFLRKKGRSRYPRA----
NICTA2-2        ----------GGSVEIPEFLRKKGRSRYPRA----
GENLU           ----------SGSVEIPEFLRKKGRSRYPRA----
LILLO           ----------GGIVEIPHFLRKKAGSRNPRA----
PHYPA1          ----------GSAINIPSFLRKRGQTRH-------
PHYPA2          ----------SSTINIPNFLRKRGQR---------

Cy-ng
ANASP           ----------KSGLDIPDFLQRRRPPKN-------
NOSSP           ----------KSGLDIPDFLQRRRPPKN-------
SYNCY           ----------APELDIPDFLQKRRFPRR-------
SYNCO           ----------GGGLDIPAFLQRKIQNRP-------
CYACA1          SARPASQPPSQTGPSRSIGSIPDFLRRFQK----------
CYAME           PNRQVTPPPPQPGPSRTIGNIPDFLRRFQK----------
GUITH           ----------------------DLWKKFY-----------
CYACA2          ----------KR---DIPDFLRRFQQENK-------
MALSP           -----DQDGKKDEEKPKGGGFRGFIKRLFS----------
```

c)

```
                                PROSITE PS01134 Ftsz_1                                  PROSITE PS01135 Ftsz_2
                                N(S,T)DxQxLx(16,18)GxG(A,T,V)G(G,S,A,N)xPx2G             PS00227 Tubulin (S,A,G)GGTG(S,A)G

ARATH1-1                        AINTDSQALLQFSAE--NPLQIGELITRGLGTGGNPLLGEQAAESKDAIANALKGSDIVFITAGMGGGTGSGAAPVVAQISKDAGILTVGVVTVPFSFEGRKRSLQA--LEAIEKLQKN
PISSA                           AINTDAQALLHSAAE---NPIKIGELITRGLGTGGNPLLGEQAAESKEAIANALKGSDLVFITAGMGGGTGSGAAPVVAQISKEAGYLTVGVVTVPFSFEGRKRSLQA--LEAIEKLQKN
NICTA1-2                        AVNTDAQALLQSTVS--NPIQIGELITRGLGTGGNPLLGEQAAESKEHIANALKGSDMVFITAGMGGGTGSGAAPVVAQIAKEAGYLTVGVVTVPFSFEGRKRSLQA--LEAIEKLQKN
NICTA1-1                        AVNTDAQALLQSTVE--NPIQIGELITRGLGTGGNPLLGEQAAESKEHIANALKGSDMVFITAGMGGGTGSGAAPVVAQIAKEAGYLTVGVVTVPFSFEGRKRSLQA--LEAIEKLQKN
NICTA1-4                        AINTDAQALLQSAAE--NPLQIGELITRGLGTGGNPLLGEQAAESKEAIANSLKGSDMVFITAGMGGGTGSGAAPVVAQIAKEAGYLTVGVVTVPFSFEGRKRSVQA--LEAIEKLQKN
NICTA1-3                        AINTDAQALLQSAAE--NPLQIGELITRGLGTGGNPLLGEQAAESKEAIANSLKGSDMVFITAGMGGGTGSGAAPVVAQIAKEAGYLTVGVVTVPFSFEGRKRSVQA--LEAIEKLQKN
TAGER                           AINTDSQALLQSVAH--NPIQIGELITRGLGTGGNPLLGEQAAESKEAIGNALKGSDIVFITAGMGGGTGSGAAPVVAQIAKEAGILTVGVVTVPFSFEGRKRSLQASALEALEKLERS
CRYSA                           AINTDSQALLNSQAQ--YPLQIGELITRGLGTGGNPNLGEQAAESKEAIANALKDSDLVFITAGMGGGTGSGAAPVVAQISKEAGYLTVGVVTVPFSFEGRKRSLQASALEALEKLERS
ORYSA                           AINTDVQALQKSQAE--HRVQIGELITRGLGTGGKPFLGEQAAESIEIIAQAVVDADLVFITAGMGGGTGSGAAPVVARVAKEAGQLTVGVVTVPFTFEGRRRSQQA--VEAIENLRKS
PHYPA3                          AVNTDKQALNKSIAP--NKIQIGQDTTAGRGAGGRSATGEEAATESLAELSWALEGADLVFITASGMGGGTGSGAAPVVARLAKAMGALTIGVITVPFTFEGFTARQA--RKAIEDMRHA
PHYPA4                          AINTDAQALLHSAAE--NPIKIGELITRGLGTGGNPLLGEQAAESKEAIADALKGSDLVFITAGMGGTGSGAAPVVAQISKEAGYLTVGVVTVPFSFEGRKRSLQA--LEAIEKLQRN
MEDTR2                          AINTDSQALVNSQAQ--HPLQIGELITRGLGTGGNPNLGEQAAESKEVIANALRDSDIVFITAGMGGGTGSGAAPVVAQIAKEAGYLTVGVVTVPFSFEGRKRSLQA--LEALEKLERS
TRIAE                           ----------------------------------------------------------FITAGMGGGTGSGAAPVVARMSKEAGNLTVGVVTVPFSFEGRRRAVQA--LEAIERLQNS
NEONI                           AINTDAQALVQSTAS--QRLQIGKQITRGLGTGGKPELGEQAAESREAIQEAANADLVFITAGMGGFGSGAAPVVARMSKEAGHLTVGVVTVPFNFEGRRRAVQA--LEAIERLQKS

FtsZ1-p1                        AINTDxQALxxFxAx  xPLQIGExITRGLGTGGNPxLGEQAAESS   (A,V) (I,V)NTDxQALxx(F,S)x(A,V)x(21,21)(L,T)GE(Q,E)
                                VV       S V     RIK K T   R A  KS T  E  T
                                            KV   Q I       R

ARATH2-1                        IVNTDIQAMRMSFVLPDNRLQIGKELITRGLGAGGNPEIGMNAARESKEVIEEALYGSDMVFVTAGMGGGTGTGAAPVIAGIAKAMGILTVGIATTPFSFEGRRRTVQA--QEGLASLRDN
ARATH2-2                        IVNTDIQAMRISFVPPDNRLQIGKELITRGLGAGGNPEIGMNAATESKEAIQEALYGSDMVFVTAGMGGGTGTGSAPIIAGVAKAMGILTVGIVTTPFSFEGRRRALQA--QEGIAALRDN
NICTA2-1                        IVNTDIQAMRMSFVAAEQRLPIGQELITRGLGAGGNPDIGMNAANESKQAIEEAVYGADMVFVTAGMGGGTGTGAAPIIAGTAKSMGILTVGIVTTPFSFEGRRRAVQA--QEGIAALREN
NICTA2-2                        IVNTDVQAIRMSFVLPENRLQIGQELITRGLGAGGNPDIGMNAANESKQAIEEAVYGADMVFVTAGMGGGTGTGSAPVIAGIAKSMGILTVGIVTTPFSFEGRRRAVQA--QEGIAALREN
GENLU                           LILLO                           IVNTDVQAIRMSFVLPENRLQIGQELITRGLGAGGNPDIGMNAAKESKVSIEESVSGADMVFVTAGMGGGTGTGSAPVIAGVAKSMGILTVGIVTTPFMFEGRRRTVQA--QEGIAALRNN
PHYPA1                          IVNTDAQAMLSFVPAQNRLQIGQKLITRGLGAGGNPEIGCSAAEESKAMVEEALRGADMVFVTAGMGGGTGSGAAPIIAGVAKQLGILTVGIVTTPFAFEGRRRSVQA--HEGIAALKNN
PHYPA2                          IVNTDAQAMASFVPAQNRLQIGQKLITRGLGAGGNPEIGCSAAEESKAMVEEALRGADMVFVTAGMGGTGSGAAPIIAGVAKQLGILTVGIVTTPFAFEGRRRSVQA--HEGIAALKNN
CHLRE                           IANTDAQAIATSFVNGKCKVQIGGKLITRGLGAGGNPEIGAKAAEESRDSIAAALQDTDMVFVTAGMGGTGSGAAPVVAQVARELGILTVGIVTTPFTFEGRQRACQA--RSALANLRAA

FtsZ2-p1                        IVNTDIQAMRxSFVxPENRLQIGKELITRGLGAGGNPEIGMNAAxES   I(V,A)NTD(I,V,A)QA(M,I,L)(R,K,A)xSFVx(23,23)IG(M,C,A)(N,S,K)
                                A  V  IK       KVP  QK              CS
                                   A  LA       G    G              AK

ANASP                           SINTDAQALTAGAP--SRLQIGQKLITRGLGAGGNPAIGQKAAEESRDEIATALEGADLVFITAGMGGTGTGAAPIVAEVAKEMGALTVGVVTRPFVFEGRRRTSQA--EQGIEGLKSR
NOSSP                           SINTDAQALTAGAP--SRLQIGQKLITRGLGAGGNPAIGQKAAEESRDEIATALEGADLVFITAGMGGTGTGAAPIVAEVAKEMGALTVGVVTRPFVFEGRRRTSQA--EQGIEGLKSR
SYNCY                           AINTDSQALTNTNAP--DCIQIGQKLITRGLGAGGNPAIGQKAAEESRDEIARSLEGTDLVFITAGMGGTGTGAAPIVAEVAKEMGCLTVGIVTRPFTFEGRRRAKQA--EEGINALQSR
SYNCO                           ALNTDAQALLHSAAP--KRMQLGQKLITRGLGAGGNPAIGKKAAEESRELIAALEGADLVFITAGMGGTGTGAAPIVAEVAKEVGALTVGIVTKPFTFEGRRRMKQA--EEGTAALQSS
AINTDVQALKRSAAH--HTLGIGNKLITRGLGAGGNPEIGRKAAEESCDQIAEAVRGADLVFVTAGMGGTGSGAAPVVAEAAREQGCLTVGVVTKPFAFEGRRRMTQA--LEAIEALRES
CYAME                           AINTDVQALKRSAAH--HTLSIGNKLITRGLGAGGNPEVGRKAAEESCDQIAEAVRGADLVFVTAGMGGTGSGAAPVVAEAARERQGCLTVGVVTKPFAFEGKRRMNQA--LEAIEALRES
GUITH                           SINTDAQALSRSLAP--NFCNIGAKLITRGLGAGGNPEIGKKAAEESRDLIAEAVSAGDLVFVTAGMGGTGSGAAPIVAEVAKEMGCLTVGVVTKPFAFEGKRRMQQA--NDAILNLRNK
CYACA2                          CINTDAQALSRVKRS--NSVTIGSEITRGLGAGGKPEVGKQAAEESQAAISSAVQGGDLVFVTAGMGGGTGSGAAPIVAKIAKEQGCLTVGVVTKPFSFEGRRRMQQA--EEAIEALRKE
MALSP                           VVNTDAQALSRSSAK--RRINIGKVLASRGLGAGGNPAIGAKAAEESREIMAVVKNADLVFVTAGMGGGTGSGAAPVVAECAKEAGALTVGVVTKPFGFEGKRRMQQA--RNAILEMKDK

FtsZ-cy-ng                      INTDAQALxxxxKAx  xxxxIGKxLITRGLGAGGNPAIGxKAAEESS   (I,V,L)NTD(A,S,V)QALxxxx(A,T)x(17,17)G(N,K)P(A,E)(I,V)Gx(K,Q)
                                V  S     T       L   IS       K EV  Q
                                L  V
```

Figure 10

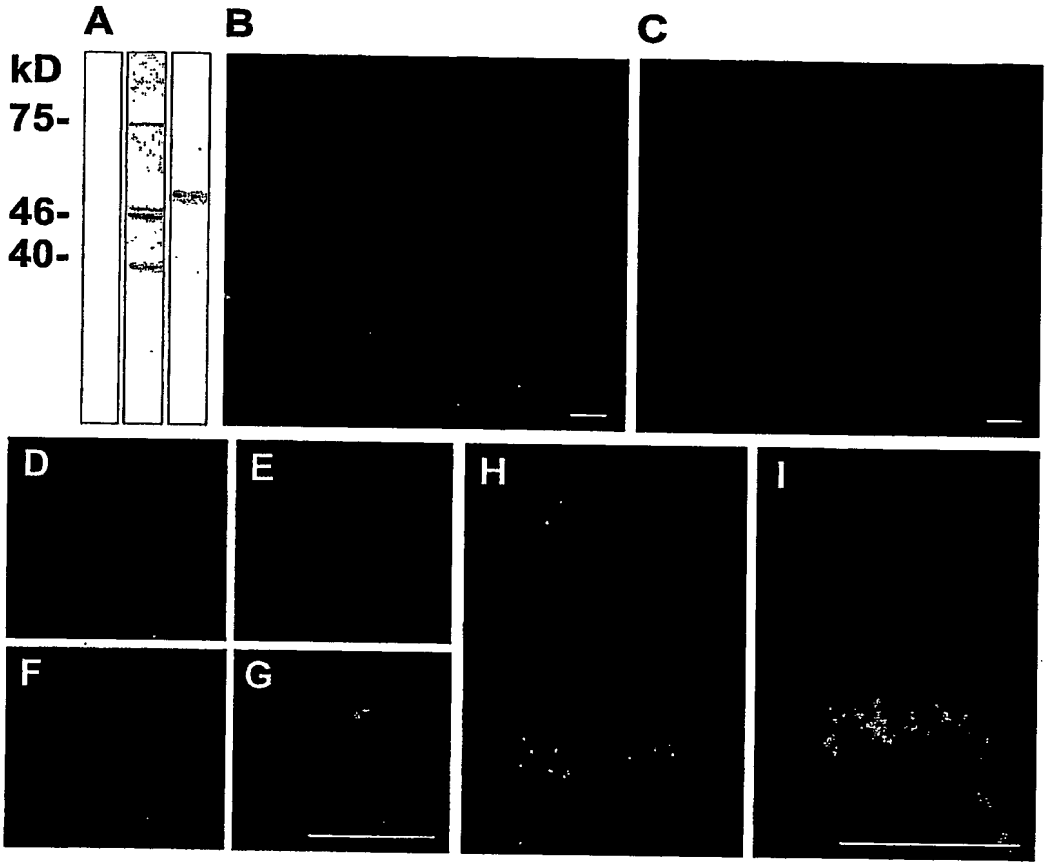
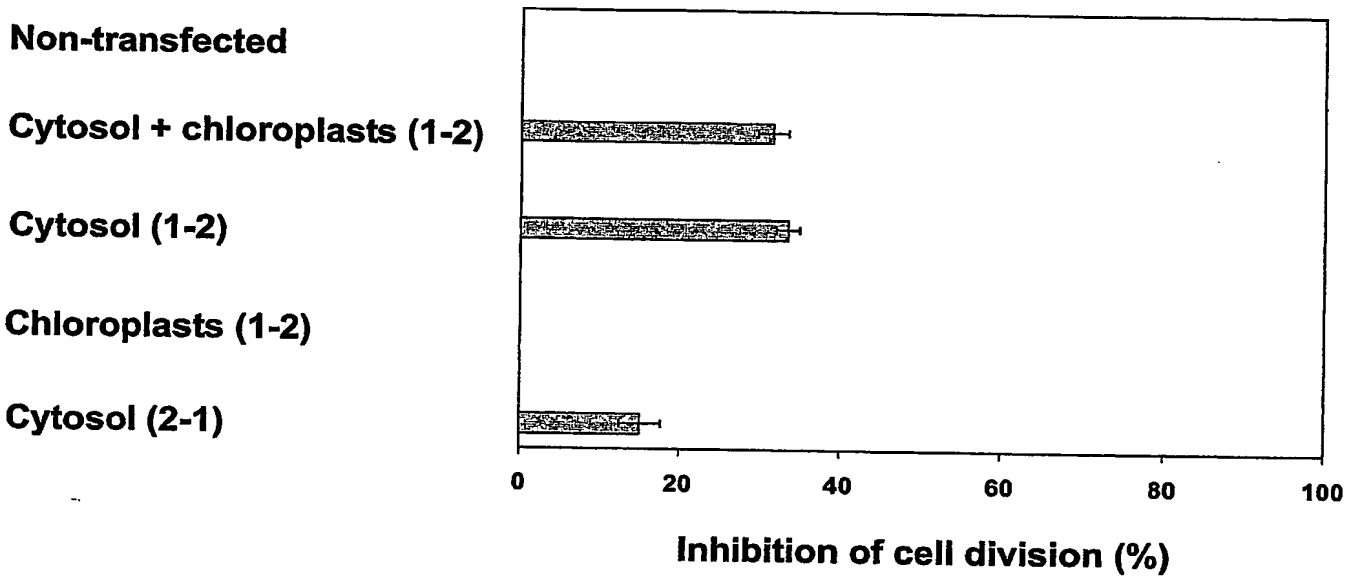


Figure 11

A

Subcellular localization of FtsZ fusion proteins



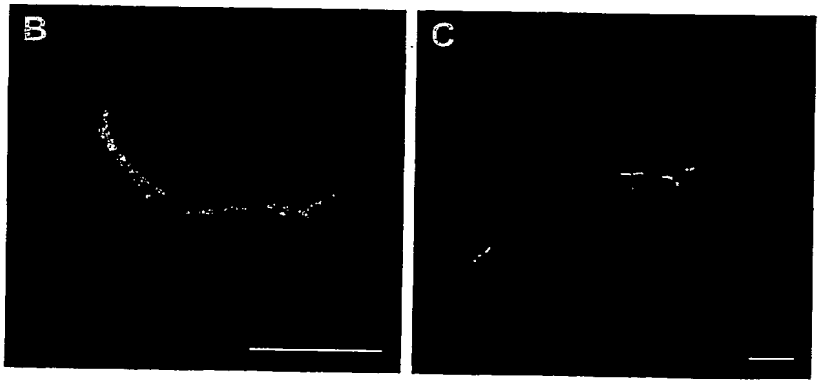


Figure 12

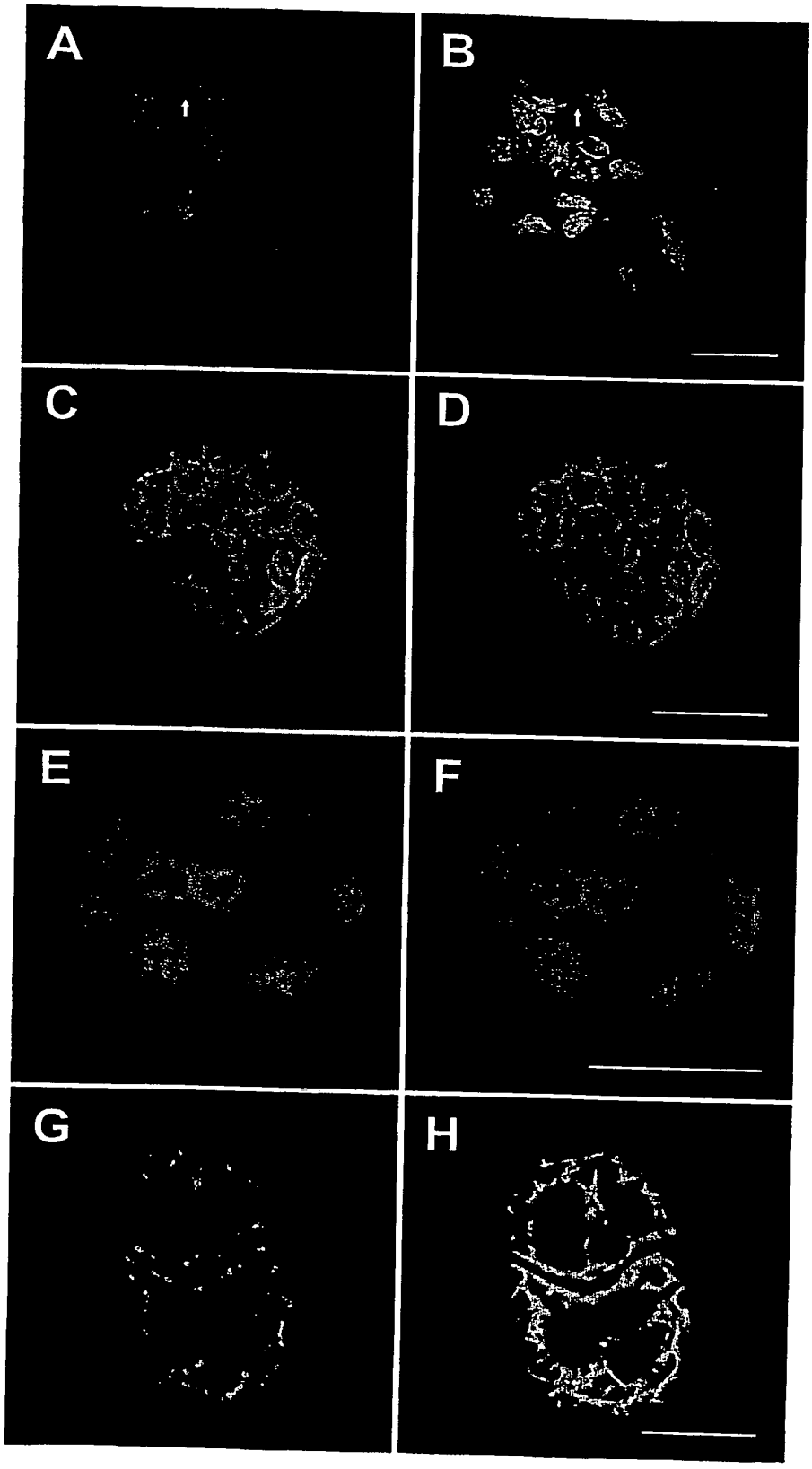


Figure 13

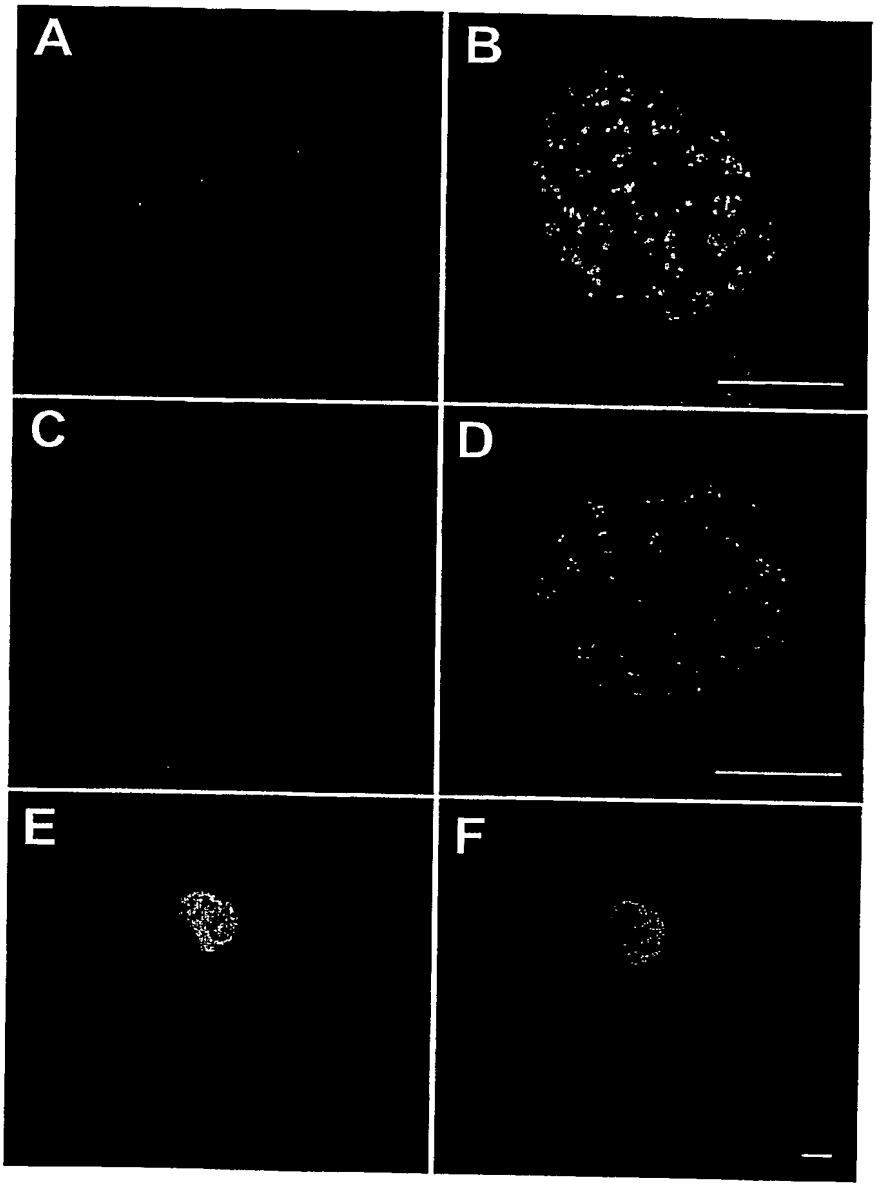


Figure 14

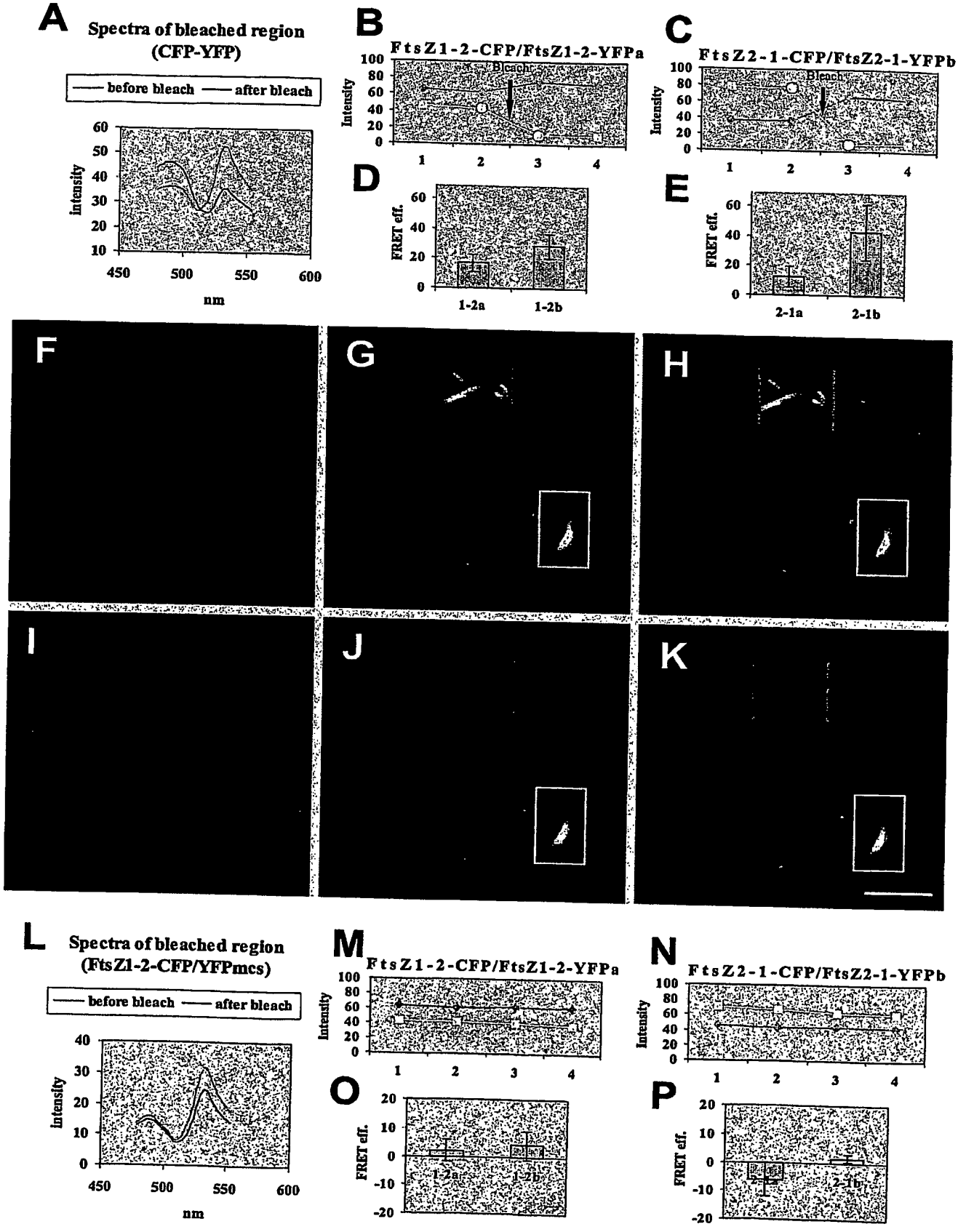
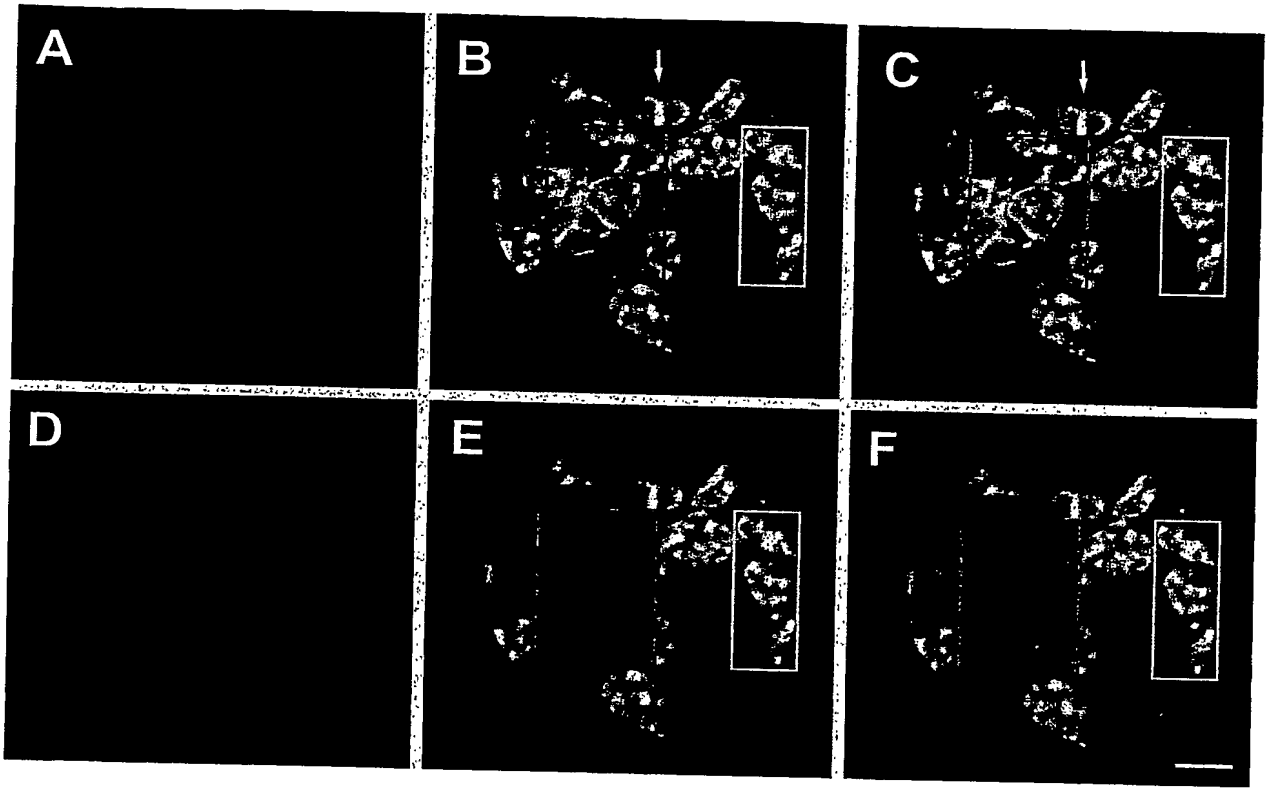
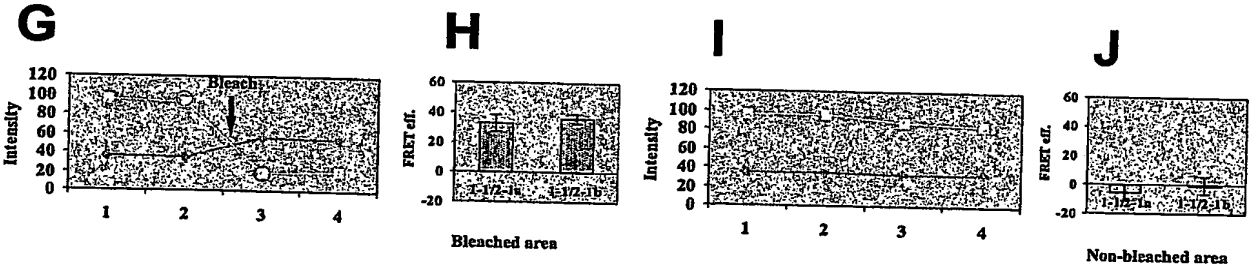
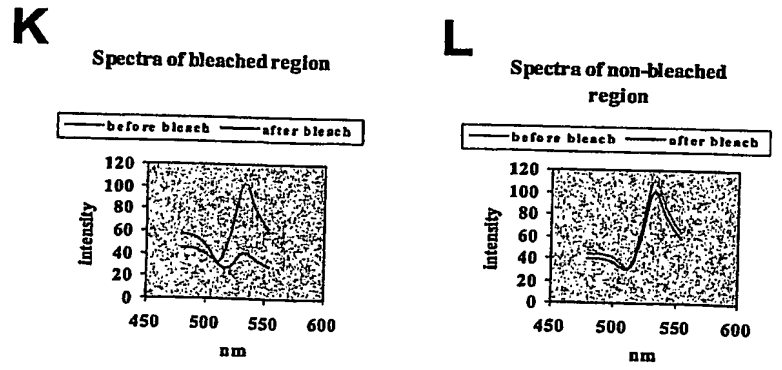

A
Spectra of bleached region (CFP-YFP)
before bleach
after bleach
Intensity
nm
B
FtsZ1-2-CFP/FtsZ1-2-YFPa
Bleach
Intensity
C
FtsZ2-1-CFP/FtsZ2-1-YFPb
Bleach
Intensity
D
FRET eff.
1-2a
1-2b
E
FRET eff.
2-1a
2-1b
F
G
H
I
J
K
L
Spectra of bleached region (FtsZ1-2-CFP/YFPmcs)
before bleach
after bleach
Intensity
nm
M
FtsZ1-2-CFP/FtsZ1-2-YFPa
Intensity
N
FtsZ2-1-CFP/FtsZ2-1-YFPb
Intensity
O
FRET eff.
1-2a
1-2b
P
FRET eff.
2-1b

Figure 15


A
B
C
D
E
F


G
Intensity
Bleach
H
FRET eff.
Bleached area
I
Intensity
J
FRET eff.
Non-bleached area


K
Spectra of bleached region
before bleach
after bleach
Intensity
nm
L
Spectra of non-bleached region
before bleach
after bleach
Intensity
nm